Certification Under 37 CFR 1.10

I hereby certify that this paper and the documents referred to as attached therein are being deposited with the United States Postal Service on the date shown below in an envelope "Express Mail Post Office to Addressee" mailing Label Number **EJ652270716US** addressed to the: Assistant Commissioner for Patents, Washington, D.C. 20231.

Denise Ortega

Name

September 27, 2001

Date

Denise Ortega

Signature

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Jan Zavada et al.

Serial No.:

Filed :

For : MN Gene and Protein

Group:

Group Art Unit:

Examiner:

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

As part of the accompanying request for filing of a divisional application under 37 CFR 1.53(b)(1), before calculating the filing fee and preliminary to the examination of the above-identified application, please amend the application as indicated below.

IN THE SPECIFICATION

Please make amendments to the Specification as indicated below.

Please replace the paragraph on page 1, lines 4-15 with the following paragraph:

This application is a divisional of U.S. Serial No. 09/178,115 (filed October 23, 1998), which will issue as U.S. Patent No. 6,297,041 on October 2, 2001, which is a continuation-in-part of U.S. Serial No. 08/787,739 (filed January 24, 1997), which issued as U.S. Patent No. 6,027,887 on February 22, 2000, which in turn is a continuation-in-part of the following seven U.S. Serial Nos., all of which were filed on June 7, 1995: U.S. Serial No. 08/485,049, which issued as U.S. Patent 6,204,370 on March 20, 2001, U.S. Serial No. 08/486,756, which issued as U.S. Patent 5,981,711 on November 9, 1999, U.S. Serial No. 08/477,504, which issued as U.S. Patent No. 5,972,353 on October 26, 1999, U.S. Serial No. 08/481,658, which issued as U.S. Patent No. 5,955,075 on September 21, 1999, U.S. Serial No. 08/485,862, which issued as U.S. Patent No. 5,989,838 on November 23, 1999, U.S. Serial No. 08/485,863, which issued as U.S. Patent No. 6,093,858 on July 25, 2000 and U.S. Serial No. 08/487,077, issued as U.S. Patent No. 6,069,242 on May 30, 2000. Those seven

applications are continuations-in-parts of now pending U.S. Serial No. 08/260,190 (filed June 15, 1994), which, in turn, is a continuation-in-part of U.S. Serial No. 08/177,093 (filed December 30, 1993), which issued as U.S. Patent No. 6,051,226 on April 18, 2000, which is in turn a continuation-in-part of U.S. Serial No. 07/964,589 (filed October 21, 1992), which issued as U.S. Patent No. 5,387,676 on February 7, 1995. This application declares priority under 35 USC § 120 from those U.S. applications and patents, and also under 35 USC § 119 from the now abandoned Czechoslovakian patent application PV-709-92 (filed March 11, 1992).

Please replace the paragraph on page 3, lines 12-25 with the following paragraph:

MN/CA IX has a number of properties that distinguish it from other known CA isoenzymes and evince its relevance to oncogenesis. Those properties include its density dependent expression in cell culture, (e.g., HeLa cells), its correlation with the tumorigenic phenotype of somatic cell hybrids between HeLa and normal human fibroblasts, its close association with several human carcinomas and its absence from corresponding normal tissues [e.g., Zavada et al., Int. J. Cancer, 54: 268-274 (1993); Pastorekova et al., Virology, 187: 620-626 (1992); Liao

et al., Am. J. Pathol., 145: 598-609 (1994); Pastorek et al., Oncogene, 9: 2788-2888 (1994); Cote, Women's Health Weekly: News Section, p. 7 (March 30, 1998); Liao et al., Cancer Res., 57: 2827 (1997); Vermylen et al., "Expression of the MN antigen as a biomarker of lung carcinoma and associated precancerous conditions," Proceedings AACR, 39: 334 (1998); McKiernan et al., Cancer Res., 57: 2362 (1997); and Turner et al., Hum. Pathol., 28(6): 740 (1997)]. In addition, the *in vitro* transformation potential of MN/CA IX cDNA has been demonstrated in NIH 3T3 fibroblasts [Pastorek et al., id.].

Please replace the paragraph on page 11, lines 23-26 with the following paragraph:

Identified herein is the location of the MN protein binding site. Also identified are MN oligopeptides that compete for attachment to cells with immobilized MN protein. Such oligopeptides prevent cell-cell adhesion and the formation of intercellular contacts.

Please replace the paragraph on page 14, lines 22-30 with the following paragraph:

A hybridoma that produces a representative MN-specific antibody, the monoclonal antibody M75 (Mab M75), was deposited at the ATCC under Number HB 11128 as indicated above. The M75

antibody was used to discover and identify the MN protein and can be used to identify readily MN antigen in Western blots, in radioimmunoassays and immunohistochemically, for example, in tissue samples that are fresh, frozen, or formalin-, alcohol-, acetone- or otherwise fixed and/or paraffin-embedded and deparaffinized. Another representative MN-specific antibody, Mab MN12, is secreted by the hybridoma MN 12.2.2, which was deposited at the ATCC under the designation HB 11647.

Please replace line 25 on page 17 with the following line:

IPTG - isopropyl-beta-D-thiogalacto-pyranoside

Please replace the paragraph on page 31, lines 7-13 with the following paragraph:

In Zavada et al., id., the isolation of a partial MN cDNA clone of 1397 bp in length was described. A lambda gt11 cDNA library of LMCV-infected HeLa cells was prepared and subjected to immunoscreening with Mab M75 in combination with goat anti-mouse antibodies conjugated with alkaline phosphatase. One positive clone was picked and subcloned into the NotI site of pBluescript KS [Stratagene; La Jolla, CA (USA)] thereby creating pBluescript-MN.

TABLE 1 on page 34, lines 1-33 has been amended as follows:

TABLE 1

Exon-Intron Structure of the Human MN Gene

Exon	Size	Genomic Position**	SEQ ID NO	5'splice acceptor	SEQ ID NO
1	445	*3507-3951	28	AGAAG gtaagt	67
2	30	5126-5155	29	TGGAG gtgaga	68
3	171	5349-5519	30	CAGTC gtgagg	69
4	143	5651-5793	31	CCGAG gtgagc	70
5	93	5883-5975	32	TGGAG gtacca	71
6	67	7376-7442	33	GGAAG gtcagt	72
7	158	8777-8934	34	AGCAG gtgggc	73
8	145	9447-9591	35	GCCAG gtacag	74
9	27	9706-9732	36	TGCTG gtgagt	75
10	82	10350-70431	37	CACAG gtatta	76
11	191	10562-10752	38	ATAAT end	

Intron	Size	Genomic Position **	SEQ ID NO	3'splice acceptor	SEQ ID NO
1	1174	3952-5125	39	atacag GGGAT	77
2	193	5156-5348	40	ccccag GCGAC	78
3	131	5520-5650	41	acgcag TGCAA	79
4	89	5794-5882	42	tttcag ATCCA	80
5	1400	5976-7375	43	ccccag GAGGG	81
6	1334	7443-8776	44	tcacag GCTCA	82
7	512	8935-9446	45	ccctag CTCCA	83
8	114	9592-9705	46	ctccag TCCAG	84
9	617	9733-10349	47	tcgcag GTGACA	85
10	130	10432-10561	48	acacag AAGGG	86

** positions are related to nt numbering in whole genomic sequence including the 5' flanking region [Figure 2A-F]

* number corresponds to transcription initiation site determined below by RNase protection assay

Please replace line 26 on page 45 with the following line:

EMSA Supershift Analysis

Please replace the paragraph on page 71, lines 27-32 with the following paragraph:

MAb M75. Monoclonal antibody M75 (MAb M75) is produced by mouse lymphocytic hybridoma VU-M75, which was initially deposited in the Collection of Hybridomas at the Institute of Virology, Slovak Academy of Sciences (Bratislava, Slovakia) and was deposited under ATCC Designation HB 11128 on September 17, 1992 at the American Type Culture Collection (ATCC). The production of hybridoma VU-M75 is described in Zavada et al., WO 93/18152.

Please replace the paragraph on page 78, lines 13-18 with the following paragraph:

The M75 MAb (or, for example, as a single chain antibody, or as its variable region) is exemplary of such a MN-specific antibody. Example 5 discloses heptapeptides (SEQ ID NOS: 107-109) that bind to the enzymatic center of the CA domain of the MN protein and, selected peptides or proteins comprising such heptapeptides would also be expected to bind to a binding site on the extracellular domain of the MN protein.

Please replace the paragraph on page 81, lines 7-15 with the following paragraph:

MN proteins and/or polypeptides may be synthesized or prepared recombinantly or otherwise biologically, to comprise one or more amino acid sequences corresponding to one or more epitopes of the MN proteins either in monomeric or multimeric form. Those proteins and/or polypeptides may then be incorporated into vaccines capable of inducing protective immunity. Techniques for enhancing the antigenicity of such polypeptides include incorporation into a multimeric structure, binding to a highly immunogenic protein carrier, for example, keyhole limpet hemocyanin (KLH), or diphtheria toxoid, and administration in combination with adjuvants or any other enhancers of immune response.

Please replace the paragraph on page 98, lines 24-30 with the following paragraph:

The MN protein is a candidate for being the product of the critical oncogene; its expression in the hybrids has been shown to correlate with their tumorigenicity [e.g., Zavada et al. (1993), supra]. The present results indicate that additional mechanisms might exist, which are able to "heal" a cancerous cell. Understanding the molecular mechanisms of action of MN

protein in normal and in tumor cells and elucidating how the reversion works may provide new approaches to cancer therapy.

Please insert the following SEQUENCE LISTING at the end of the Specification on page 117 beginning a new page

SEQUENCE LISTING

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Pastorekova, Silvia
Pastorek, Jaromir

<120> MN Gene and Protein

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Met Pro Val His Pro
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<210> 9
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<221> inosine
<222> (36)..(37) (41)..(42) (46)..(47)
<223> each of the modified_bases at positions (36), (37), (41), (42), (46) and (47) are inosine

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1 5

<210> 11

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<210> 12
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<303> DNA Sequencing and Mapping
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<307> 1990

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<223> sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as motif frequently found in gene regulatory proteins.

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<223> variants in sequence element defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as motif frequently found in gene regulatory proteins.

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<220>
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<223> 7th MN exon

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<220>
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<222> (1)
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<223> 11th MN exon

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actcaggact gaagtgccca ctcacttttt tttttttttt ttttgagaca aactttcact 660
tttgttgccc aggctggagt gcaatggcgc gatctcggct cactgcaacc tccacctccc 720
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ccaccacgcc cggctaattt ttgtattttt agtagagacg gggtttcgcc atgttggtca 840
ggctggtctc gaactcctga tctcaggtga tccaaccacc ctggcctccc aaagtgctgg 900
gattataggc gtgagccaca gcgcctggcc tgaagcagcc actcactttt acagacccta 960
agacaatgat tgcaagctgg taggattgct gtttggccca cccagctgcg gtgttgagtt 1020
tgggtgcggt ctcctgtgct ttgcacctgg cccgcttaag gcatttgtta cccgtaatgc 1080
tcctgtaagg catctgcgtt tgtgacatcg ttttggtcgc caggaaggga ttggggctct 1140

aagcttgagc ggttcatcct tttcatttat acag 1174

<210> 40
<211> 193
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(193)
<223> 2nd MN intron

<400> 40
gtgagacacc cacccgctgc acagacccaa tctgggaacc cagctctgtg gatctcccct 60
acagccgtcc ctgaacactg gtcccgggcg tcccacccgc cgcccaccgt cccacccct 120
cacctttctt acccgggttc cctaagttcc tgacctaggc gtcagacttc ctcactatac 180
tctcccaccc cag 193

<210> 41
<211> 131
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

<400> 41
gtgagggggt ctccccgccg agacttgggg atggggcggg gcgcagggaa gggaaccgtc 60
gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc ggggccggct cacttgcctc 120
tccctacgca g 131

<210> 42
<211> 89
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(89)
<223> 4th MN intron

<400> 42
gtgagcgcgg actggccgag aaggggcaaa ggagcggggc ggacgggggc cagagacgtg 60
gccctctcct accctcgtgt ccttttcag 89

<210> 43
<211> 1400
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1400)
<223> 5th MN intron

<400> 43
gtaccagatc ctggacaccc cctactcccc gctttcccat cccatgctcc tcccggactc 60
tatcgtggag ccagagaccc catcccagca agctcactca ggcccctggc tgacaaactc 120
attcacgcac tgtttgttca tttaacaccc actgtgaacc aggcaccagc ccccaacaag 180
gattctgaag ctgtaggtcc ttgcctctaa ggagcccaca gccagtgggg gaggctgaca 240
tgacagacac ataggaagga catagtaaag atggtggtca cagaggaggt gacacttaaa 300
gccttcactg gtagaaaaga aaaggaggtg ttcattgcag aggaaacaga atgtgcaaag 360
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aaagggaagg gatggtgaga tgcctgctag gttcactcac tcacttttat ttatttattt 480
atttttttga cagtctctct gtcgcccagg ctggagtgca gtggtgtgat cttgggtcac 540
tgcaacttcc gcctcccggg ttcaagggat tctcctgcct cagcttcctg agtagctggg 600
gttacaggtg tgtgccacca tgcccagcta attttttttt gtatttttag tagacagggt 660
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gattttaaga gggagacact gtctctaaaa aaaaaaacaa cagcaacaac aaaaagcaac 1260
aaccattaca atttatgtt ccctcagcat tctcagagct gaggaatggg agaggactat 1320
gggaaccccc ttcatgttcc ggccttcagc catggccctg gatacatgca ctcatctgtc 1380
ttacaatgtc attcccccag 1400

<210> 44
<211> 1334
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1334)
<223> 6th MN intron

<400> 44
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gagcttcagg tctgaggctg gagatgggct ccctccagtg caggagggat tgaagcatga 120
gccagcgctc atcttgataa taaccatgaa gctgacagac acagttaccc gcaaacggct 180
gcctacagat tgaaaaccaa gcaaaaaccg ccgggcacgg tggctcacgc ctgtaatccc 240
agcactttgg gaggccaagg caggtggatc acgaggtcaa gagatcaaga ccatcctggc 300
caacatggtg aaaccccatc tctactaaaa atacgaaaaa atagccaggc gtggtggcgg 360
gtgcctgtaa tcccagctac tcgggaggct gaggcaggag aatggcatga acccgggagg 420
cagaagttgc agtgagccga gatcgtgcca ctgcactcca gcctgggcaa cagagcgaga 480
ctcttgtctc aaaaaaaaaa aaaaaaaaga aaaccaagca aaaaccaaaa tgagacaaaa 540
aaaacaagac caaaaaatgg tgtttggaaa ttgtcaaggt caagtctgga gagctaaact 600
tttctgaga actgtttatc tttaataagc atcaaatatt ttaactttgt aaatactttt 660
gttggaaatc gttctcttct tagtcactct tgggtcattt taaatctcac ttactctact 720
agacctttta ggtttctgct agactaggta gaactctgcc tttgcatttc ttgtgtctgt 780
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caggctgctc tcaaactcct gaccttgtga tccaccagcc tcggcctccc aaagtgctgg 960
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aactgtatcc ctataccctg aagctttaag ggggtgcaat gtagatgaga ccccaacata 1320
gatcctcttc acag 1334

<210> 45
<211> 512
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(512)
<223> 7th MN intron

<400> 45
gtgggcctgg ggtgtgtgtg gacacagtgg gtgcggggga aagaggatgt aagatgagat 60
gagaaacagg agaagaaaga aatcaaggct gggctctgtg gcttacgcct ataatcccac 120
cacgttggga ggctgaggtg ggagaatggt ttgagcccag gagttcaaga caaggcgggg 180
caacatagtg tgaccccatc tctaccaaaa aaaccccaac aaaaccaaaa atagccgggc 240

atggtggtat gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300
ttccaggagt ttgagactgc agtgagctat gatcccacca ctgcctacca tctttaggat 360
acatttattt atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420
tggagccctg aggtgctggt tgtgagctgg cctgggaccc ttgtttcctg tcatgccatg 480
aacccaccca cactgtccac tgacctccct ag 512

<210> 46
<211> 114
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(114)
<223> 8th MN intron

<400> 46
gtacagcttt gtctggtttc cccccagcca gtagtccctt atcctcccat gtgtgtgcca 60
gtgtctgtca ttggtggtca cagcccgcct ctcacatctc ctttttctct ccag 114

<210> 47
<211> 617
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(617)
<223> 9th MN intron

<400> 47
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agggctgctc aggaccgcct ctgctccctc tccttttctg cagaacagac cccaacccca 120
atattagaga ggcagatcat ggtggggatt cccccattgt ccccagaggc taattgatta 180
gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatccccc cccctttttt 240
taaagatagg gtctcactct gtttgcccca ggctggggtg ttgtggcacg atcatagctc 300
actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360
ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420
aagcaaaaac ggtgcttatc ttaccccttc tcgtgtatcc accctcatcc cttggctggc 480
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tgcactgagg caggtgttga ggaactctgc agacccctct tccttcccaa agcagccctc 600
tctgctctcc atcgcag 617

<210> 48
<211> 130
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

<400> 48
gtattacact gaccctttct tcaggcacaa gcttccccca cccttgtgga gtcacttcat 60
gcaaagcgca tgcaaatgag ctgctcctgg gccagttttc tgattagcct ttcctgttgt 120
gtacacacag 130

<210> 49
<211> 1401
<212> DNA
<213> HUMAN

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctcactgcaa 60
cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120
tacaggcatg cgccaccacg cccggctaat ttttgtattt ttagtagaga cggggtttcg 180
ccatgttggt caggctggtc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240
ccaaagtgct gggattatag gcgtgagcca cagcgcctgg cctgaagcag ccactcactt 300
ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc cacccagctg 360
cggtgttgag tttgggtgcg gtctcctgtg ctttgcacct ggcccgctta aggcatttgt 420
tacccgtaat gctcctgtaa ggcatctgcg tttgtgacat cgttttggtc gccaggaagg 480
gattggggct ctaagcttga gcggttcatc cttttcattt atacagggga tgaccagagt 540
cattggcgct atggaggtga gacacccacc cgctgcacag acccaatctg ggaacccagc 600
tctgtggatc tcccctacag ccgtccctga acactggtcc cgggcgtccc acccgccgcc 660
caccgtccca ccccctcacc ttttctaccc gggttcccta agttcctgac ctaggcgtca 720
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ttgacgaggc cttggggcgc ccgggaggcc tggccgtgtt ggccgccttt ctggaggtac 1380
cagatcctgg acacccccta c 1401

<210> 50
<211> 59
<212> PRT
<213> HUMAN

<400> 50
Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
1   5   10   15

Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
            20   25   30

Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
        35   40   45

Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
    50   55

<210> 51
<211> 257
<212> PRT
<213> HUMAN

<400> 51
Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
1   5   10   15

Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
            20   25   30

Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
        35   40   45

Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
    50   55   60

Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
65   70   75   80

Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly
                85   90   95

Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe
            100   105   110

Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
115 120 125

Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe
130 135 140

Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser
145 150 155 160

Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly
165 170 175

Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln
180 185 190

Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp
195 200 205

Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr
210 215 220

Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225 230 235 240

Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
245 250 255

Pro

<210> 52
<211> 20
<212> PRT
<213> HUMAN

<400> 52
Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
1 5 10 15

Phe Leu Val Gln
20

<210> 53
<211> 25

<212> PRT
<213> HUMAN

<400> 53
Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1   5   10   15

Pro Ala Glu Val Ala Glu Thr Gly Ala
            20   25

<210> 54
<211> 59
<212> PRT
<213> HUMAN

<400> 54
Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
1   5   10   15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
            20   25   30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
        35   40   45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
    50   55

<210> 55
<211> 470
<212> RNA
<213> HUMAN

<400> 55
cauggccccg auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60
gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120
cugcaaaagg gcgcucugug agucagccug cuccccucca ggcuugcucc ucccccaccc 180
agcucucguu uccaaugcac guacagcccg uacacaccgu gugcugggac accccacagu 240
cagccgcaug gcucccccugu gccccagccc cuggcucccu cuguugaucc cggccccugc 300
uccaggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucccca 360
gagguugccc cggaugcagg aggauucccc cuugggagga ggcucuucug gggaagauga 420
cccacugggc gaggaggauc ugcccaguga agaggauuca cccagagagg 470

<210> 56
<211> 292
<212> DNA
<213> HUMAN

<400> 56
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ctcggctcac tgcaagctcc acctcccgag ttcacgccat tttcctgcct cagcctcccg 120
agtagctggg actacaggcg cccgccacca tgcccggcta atttttgta tttttggtag 180
agacggggtt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240
gcctcggcct cccaaagttc tgggattaca ggtgtgagcc accgcacctg gc 292

<210> 57
<211> 262
<212> DNA
<213> HUMAN

<400> 57
tttcttttt gagacagggt cttgctctgt cacccaggcc agagtgcaat ggtacagtct 60
cagctcactg cagcctcaac cgcctcggct caaaccatca tcccatttca gcctcctgag 120
tagctgggac tacaggcaca tgccattaca cctggctaat tttttgtat ttctagtaga 180
gacagggttt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240
cacctcagcc tcccaaaatg ag 262

<210> 58
<211> 2501
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(2501)
<223> region 5' to transcription initiation site as determined by RNase protection assay (nucleotide 3507 of Figures 2A-2F and of SEQ ID NO: 5), corresponding to region of SEQ ID NO: 5 and Figures 2A-2F from nucleotide (7) to nucleotide (2507), in which region some regulatory elements are probably situated.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of base at position 1968, which is the same unknown base as that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and

unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5' region flanking the transcription initiation site (3507) as determined by RNase protection assay.

<400> 58
tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60
agggttaaat ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttaaaa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540
taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720
atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780
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gtattttttgg tagagacggg gtttcaccgt gttagccaga atggtctcga tctcctgact 1140
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gatattgaca gggtttgccc tcactcacta gattgtgagc tcctgctcag ggcaggtagc 2340
gtttttttgtt tttgtttttg tttttctttt ttgagacagg gtcttgctct gtcacccagg 2400
ccagagtgca atggtacagt ctcagctcac tgcagcctca accgcctcgg ctcaaaccat 2460

catcccattt cagcctcctg agtagctggg actacaggca c 2501

<210> 59
<211> 292
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)

<400> 59
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gtagctggga ctacaggcgc ccgccaccat gcccggctaa ttttttgtat ttttggtaga 180
gacggggttt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccacccg 240
cctcggcctc ccaaagttct gggattacag gtgtgagcca ccgcacctgg cc 292

<210> 60
<211> 262
<212> DNA
<213> HUMAN

<400> 60
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agctcactgc agcctcaacc gcctcggctc aaaccatcat cccatttcag cctcctgagt 120
agctgggact acaggcacat gccattacac ctggctaatt tttttgtatt tctagtagag 180
acagggtttg gccatgttgc ccgggctggt ctcgaactcc tggactcaag caatccaccc 240
acctcagcct cccaaaatga gg 262

<210> 61
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<212> DNA
<213> HUMAN

<400> 61
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aagtagctgc gattacaggc atgcgccacc acgcccggct aatttttgta tttttagtag 180
agacggggtt tcgccatgtt ggtcaggctg gtctcgaact cctgatctca ggtgatccaa 240
ccaccctggc ctcccaaagt gctgggatta taggcgtgag ccacagcgcc tggc 294

<210> 62
<211> 276
<212> DNA
<213> HUMAN

<400> 62
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gtgtgtgcca ccatgcccag ctaatttttt tttgtatttt tagtagacag ggtttcacca 180
tgttggtcag gctggtctca aactcctggc ctcaagtgat ccgcctgact cagcctacca 240
aagtgctgat tacaagtgtg agccaccgtg cccagc 276

<210> 63
<211> 289
<212> DNA
<213> HUMAN

<400> 63
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aaatacgaaa aaatagccag gcgtggtggc gggtgcctgt aatcccagct actcgggagg 180
ctgaggcagg agaatggcat gaacccggga ggcagaagtt gcagtgagcc gagatcgtgc 240
cactgcactc cagcctgggc aacagagcga gactcttgtc tcaaaaaaa 289

<210> 64
<211> 298
<212> DNA
<213> HUMAN

<400> 64
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caaaaaaacc ccaacaaaac caaaaatagc cgggcatggt ggtatgcggc ctagtcccag 180
ctactcaagg aggctgaggt gggaagatcg cttgattcca ggagtttgag actgcagtga 240
gctatgatcc caccactgcc taccatcttt aggatacatt tatttattta taaaagaa 298

<210> 65
<211> 105
<212> DNA
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<400> 65
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ctgaccttgt gatccaccag cctcggcctc ccaaagtgct gggat 105

<210> 66
<211> 83
<212> DNA
<213> HUMAN

<400> 66
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aggcatgagc cactgtgcct ggc 83

<210> 67
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<212> DNA
<213> HUMAN

<400> 67
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<210> 68
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<212> DNA
<213> HUMAN

<400> 68
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<210> 69
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<213> HUMAN

<400> 69
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<400> 70

ccgaggtgag c 11

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tggaggtacc a 11

<210> 72
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<212> DNA
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<400> 72
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<400> 75
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<400> 76
atacagggga t 11

<210> 77
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<212> DNA
<213> HUMAN

<400> 77
atacagggga t 11

<210> 78
<211> 11
<212> DNA
<213> HUMAN

<400> 78
ccccaggcga c 11

<210> 79
<211> 11
<212> DNA
<213> HUMAN

<400> 79
acgcagtgca a 11

<210> 80
<211> 11
<212> DNA
<213> HUMAN

<400> 80
tttcagatcc a 11

<210> 81
<211> 11
<212> DNA
<213> HUMAN

<400> 81
ccccaggagg g 11

<210> 82
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<400> 82
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<210> 84
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<213> HUMAN

<400> 84
ctccagtcca g 11

<210> 85
<211> 12
<212> DNA
<213> HUMAN

<400> 85
tcgcaggtga ca 12

<210> 86

<211> 11
<212> DNA
<213> HUMAN

<400> 86
acacagaagg g 11

<210> 87
<211> 377
<212> PRT
<213> HUMAN

<400> 87
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20 25 30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
35 40 45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
50 55 60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
65 70 75 80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
85 90 95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
100 105 110

Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
115 120 125

Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
130 135 140

Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
145 150 155 160

Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
165 170 175

Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
180 185 190

Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
195 200 205

Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
210 215 220

Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
225 230 235 240

Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
245 250 255

Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
260 265 270

Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
275 280 285

Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
290 295 300

Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
305 310 315 320

Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
325 330 335

Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
340 345 350

Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
355 360 365

Leu Asn Ser Cys Leu Ala Ala Gly Asp
370 375

<210> 88
<211> 34
<212> DNA
<213> HUMAN

<400> 88

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<210> 89
<211> 34
<212> DNA
<213> HUMAN

<400> 89
attcctctag acagttaccg gctccccctc agat 34

<210> 90
<211> 3532
<212> DNA
<213> HUMAN

<220>
<221> misc_feature which includes the MN gene promoter
<222> (1)..(3532)
<223> region including the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter, and corresponds to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 1968
<222> (1968)
<223> unsure of the base at position 1968, which is the same unknown base at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence), position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That unknown base is in the region that includes the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter.

<400> 90
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gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttaaaa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540

taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720
atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780
gtaggtactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtac 840
tggcctttat ctgtaatatg ggcatattta atacaatata atttttggag tttttttgtt 900
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aaagggcgct ctgtgagtca gcctgctccc ctccaggctt gctcctcccc cacccagctc 3480
tcgtttccaa tgcacgtaca gcccgtacac accgtgtgct gggacacccc ac 3532

<210> 91
<211> 204
<212> DNA
<213> HUMAN

<400> 91
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caaacctgtg agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120
ccctccaggc ttgctcctcc cccacccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg ctgggacacc ccac 204

<210> 92
<211> 132
<212> DNA
<213> HUMAN

<400> 92
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gcactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg 120
aaggcagcat gc 132

<210> 93
<211> 275
<212> DNA
<213> HUMAN

<400> 93
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tcagcctgct cccctccagg cttgctcctc ccccacccag ctctcgtttc caatgcacgt 240
acagcccgta cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

<400> 94
ctgctcccct ccaggcttgc tcctccccca cccagctctc gtttccaatg cacgtacagc 60
ccgtacacac cgtgtgctgg gacacccca 89

<210> 95
<211> 61
<212> DNA
<213> HUMAN

<400> 95
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a 61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
acctgcccct cactccaccc ccatcctagc tttggtatgg gggagagggc acagggccag 60
acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
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Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
20 25 30

Glu Asp Leu Pro
35

<210> 98
<211> 6
<212> PRT
<213> HUMAN

<400> 98
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1 5

<210> 99
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<400> 99
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<210> 100
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<212> PRT
<213> HUMAN

<400> 100
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<210> 101
<211> 6
<212> PRT
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<400> 101
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1 5

<210> 102
<211> 7
<212> PRT
<213> HUMAN

<400> 102
Glu Glu Asp Leu Pro Ser Glu
1 5

<210> 103

<211> 6
<212> PRT
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<400> 103
Asp Leu Pro Gly Glu Glu
1 5

<210> 104
<211> 22
<212> PRT
<213> HUMAN

<400> 104
Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro
1 5 10 15

Ser Glu Glu Asp Ser Pro
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<210> 105
<211> 25
<212> PRT
<213> HUMAN

<400> 105
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1 5 10 15

Pro Pro Gly Glu Glu Asp Leu Pro Gly
20 25

<210> 106
<211> 24
<212> PRT
<213> HUMAN

<400> 106
Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10 15

Gly Glu Glu Asp Leu Pro Glu Val
20

<210> 107
<211> 7
<212> PRT
<213> HUMAN

<400> 107
Gly Glu Thr Arg Ala Pro Leu
1 5

<210> 108
<211> 7
<212> PRT
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<400> 108
Gly Glu Thr Arg Glu Pro Leu
1 5

<210> 109
<211> 7
<212> PRT
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<400> 109
Gly Gln Thr Arg Ser Pro Leu
1 5

<210> 110
<211> 1247
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1247)
<223> region 5' to the transcription initiation site as determined by RNase protection assay (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) in which an activating element is localized, which region corresponds to nucleotide 1328 to nucleotide 2574 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>
<221> unsure what base is at position 647

<222> (647)
<223> unsure of the base at position 647, which is the same unknown base as that at position 1974 of SEQ ID NO: 5, and as that at position 1968 of SEQ ID NOS: 58 and 90. That unknown base at position 647 is in a region in which an activating element is localized and is 5' to the transcription initiation site.

<400> 110
tatgctactt tttgcagtcc tttcattaca tttttctctc ttcatttgaa gagcatgtta 60
tatcttttag cttcacttgg cttaaaaggt tctctcatta gcctaacaca gtgtcattgt 120
tggtaccact tggatcataa gtggaaaaac agtcaagaaa ttgcacagta atacttgttt 180
gtaagaggga tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga 240
ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactattt 300
ttcttaagca agatatgcta aagttttgtg agccttttc cagagagagg tctcatatct 360
gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg 420
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aatctcaatt ctgtcagaat tggtacaaga aatagctgct atgtttcttg acattccact 600
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ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagaggtgag gcattcttaa 720
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ggcgcagtgg ctcacacctg taatcccagc actttgggtg gccaaggtgg aaggatcaaa 900
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cagagtgcaa tggtacagtc tcagctcact gcagcctcaa ccgcctcggc tcaaaccatc 1140
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ttttttgta tttctagtag agacagggtt tggccatgtt gcccggg 1247

<210> 111
<211> 17
<212> DNA
<213> HUMAN

<400> 111
ctctgtgagt cagcctg 17

<210> 112
<211> 23
<212> DNA
<213> HUMAN

<400> 112

aggcttgctc ctcccccacc cag 23

<210> 113
<211> 18
<212> DNA
<213> HUMAN

<400> 113
agactttggc tccatctc 18

<210> 114
<211> 20
<212> DNA
<213> HUMAN

<400> 114
cactccaccc ccatcctagc 20

<210> 115
<211> 26
<212> DNA
<213> HUMAN

<400> 115
gggagagggc acagggccag acaaac 26

<210> 116
<211> 20
<212> PRT
<213> HUMAN

<400> 116
```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1               5                  10                  15

Gly Gly Gly Ser
            20
```

IN THE CLAIMS

Please cancel Claims 1-21, 28 and 29. Please amend the claims as follows.

Please replace Claim 22 with the following new Claim 22:

22. (Amended) An anti-idiotype antibody to an antibody which specifically binds to an MN protein, wherein said MN protein is encoded by a nucleic acid selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) polynucleotides that hybridize under stringent conditions to SEQ ID NO: 1's complement; and

(c) polynucleotides that differ from SEQ ID NO: 1 or from the polynucleotide sequences of (b) due to the degeneracy of the genetic code.

Please replace Claim 23 with the following new Claim 23:

23. (Amended) An anti-idiotype antibody according to Claim 22, wherein said antibody that is specific for said MN protein, is either the M75 monoclonal antibody secreted from the hybridoma VU-M75, which was deposited at the American Type Culture Collection under ATCC No. HB 11128, or the MN12 monoclonal antibody that is secreted from the hybridoma MN

12.2.2, which was deposited at the American Type Culture Collection under ATCC No. HB 11647.

Please add new Claims 30-52.

30. An anti-idiotype antibody to an antibody which specifically binds to an MN polypeptide, wherein said MN polypeptide is encoded by a nucleic acid that comprises a polynucleotide containing at least 29 nucleotides, said nucleic acid being selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) polynucleotides that hybridize under stringent conditions to SEQ ID NO: 1's complement; and

(c) polynucleotides that differ from SEQ ID NO: 1 or from the polynucleotide sequences of (b) due to the degeneracy of the genetic code.

31. The anti-idiotype antibody according to Claim 30, wherein said antibody that is specific to said MN polypeptide is either the M75 monoclonal antibody secreted from the hybridoma VU-M75, which was deposited at the American Type Culture Collection under ATCC No. HB 11128, or the MN12 monoclonal antibody that is secreted from the hybridoma MN 12.2.2, which was

deposited at the American Type Culture Collection under ATCC No. HB 11647.

32. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 30.

33. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 31.

34. An anti-anti-idiotype antibody according to Claim 32 which is polyclonal.

35. An anti-anti-idiotype antibody according to Claim 33 which is polyclonal.

36. The anti-idiotype antibody according to Claim 30 wherein said nucleic acid comprises a polynucleotide containing at least 50 nucleotides.

37. The anti-idiotype antibody according to Claim 30 wherein said polynucleotide comprises at least 100 nucleotides.

38. The anti-idiotype antibody according to Claim 30 wherein said nucleic acid comprises a polynucleotide containing at least 150 nucleotides.

39. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 36.

40. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 37.

41. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 38.

42. An anti-idiotype antibody to an antibody which specifically binds to an MN polypeptide, wherein said MN polypeptide is encoded by a nucleic acid that comprises a polynucleotide containing at least 25 nucleotides, said nucleic acid being selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) polynucleotides that hybridize under stringent conditions to SEQ ID NO: 1's complement; and

(c) polynucleotides that differ from SEQ ID NO: 1 or from the polynucleotide sequences of (b) due to the degeneracy of the genetic code.

43. The anti-idiotype antibody according to Claim 42 wherein said nucleic acid comprises a polynucleotide containing at least 27 nucleotides.

44. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 42.

45. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 43.

46. The anti-idiotype antibody according to Claim 22 wherein said MN protein is encoded by SEQ ID NO: 1 or by a fragment of SEQ ID NO: 1.

47. The anti-idiotype antibody according to Claim 30 wherein said MN polypeptide is encoded by a fragment of SEQ ID NO: 1.

48. The anti-idiotype antibody according to Claim 42 wherein said MN polypeptide is encoded by a fragment of SEQ ID NO: 1.

49. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 46.

50. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 47.

51. An anti-anti-idiotype antibody to the anti-idiotype antibody according to Claim 48.

52. The anti-idiotype antibody according to Claim 22 wherein said stringent hybridization conditions comprise 50% formamide at 42 degrees C.

REMARKS

To assist in the examination of this application and as required by 37 CFR 1.121, enclosed herewith as Appendix 1 is a marked up version of the changes made to the specification and claims to indicate how the previous version of the specification has been modified to produce the clean replacement paragraphs.

The modifications are indicated by underlining and in bold type for additions, and by strikeouts for deletions. Also enclosed as Appendix 2 is a clean set of all the claims now pending the accordance with 37 CFR 1.121(c)(3).

Specification

The Specification has been amended to claim priority from the parent, grandparent, great-grandparent, great-great grandparent and great-great-great-grandparent applications and to update the status of those priority applications. The Specification has also been amended to correct a number of typographical/proofreading errors.

The Specification at page 3 has been amended to correct a typographical/proofreading error in the year of publication of an article by Zavada et al., in the International Journal of Cancer. The Specification has also been amended to correct other obvious typographical/proofreading errors.

The Specification has been amended in Table 1, line 5, page 34 in order to replace "Intron" with "Exon". Page 33, lines 20-25 reads as follows:

> Exon-Intron Structure of Complete MN Genomic Region
>
> The complete sequence of the overlapping clones contains 10,898 bp (SEQ ID NO: 5). Figure 5 depicts the organization of the

human MN gene, showing the location of all 11 exons as well as the 2 upstream and 6 intronic Alu repeat elements. All the exons are small, ranging from 27 to 191 bp, with the exception of the first exon which is 445 bp. The intron sizes range from 89 to 1400 bp.

[Emphasis added.] As the above quote shows, the MN gene contains 11 exons, and that the first exon contains 445 base pairs. The top section of Table 1 depicts 11 regions wherein the first region contains 445 base pairs. Further, the same Table 1 can be found in many of the issued MN patents including U.S. Patent 5,972,353. Table 1 (at column 18) of U.S. Patent No. 5,972,353 reads "Exon" on its fifth line. Applicants respectfully submit that the amendment at page 34 of the instant application corrects a typographical, proofreading error that would be obvious to those of skill in the art.

Claims

Applicants have canceled Claims 1-21, 28 and 29 in that the instant application is a divisional of its parent application - U.S. Serial No. 09/178,115. The parent application was subject to a 5-way Election/Restriction Requirement mailed from the U.S. Patent and Trademark Office (PTO) on June 21, 2000. The claims of the instant application are based upon the Group II claims of that Election/Restriction Requirement ["II. Claims 9-11 and 22-

27, drawn to a MN-specific antibody, classified in class 530, subclass 387.1."]

Appendix 1 shows the amendments made to Claims 22-27 of the parent application. Applicants respectfully submit that those amendments and the addition of new Claims 30-52 are made to point out with more particularity and clarity the subject matter regarded by the Applicants as their invention, and that no new subject matter has been added by those amendments and new claims.

Support in the Specification concerning anti-idiotype antibodies to MN-specific antibodies and anti-anti-idiotype antibodies to such anti-idiotype antibodies can be found at least at page 12, line 29 to page 13, line 31; at page 15, lines 24-33; at page 75, line 11 to page 76, line 21; at page 81, lines 27-32; and at page 122, lines 9-12.

The amendment to Claim 22 specifies with particularity and clarity the term "MN-specific antibody," and that terminology reflected in new Claims 30-52 is supported throughout the Specification, e.g., at least at page 7, line 12 to page 15, line 14; more specifically, e.g., at least at page 7, lines 12-20, at page 9, lines 18-24, at page 10, lines 15-24, at page 12, lines 29-31, at page 13, lines 12-18, at page 13, lines 27-31 and at page 14, lines 4-5.

Stringent hybridization conditions, to which independent Claims 22, 30 and 42 refer, are described and exemplified in the Specification at least at page 60, line 6 to page 61, line 10. Specifically, the condition of "50% formamide at 42 degrees C" of new Claim 52 is supported at least at page 60, lines 13-19, at page 7, lines 12-21 and at page 8, lines 7-20.

The terms "protein" and "polypeptide" of the instant claims are defined in the Specification at page 53, lines 7-10. Whereas "polypeptide" is composed of "50 or less amino acids," "a protein" is "composed of more than 50 amino acids."

The phrases concerning "a polynucleotide containing" different numbers of nucleotides -- "at least 29 nucleotides" (Claim 30), "at least 50 nucleotides" (Claim 36), "at least 100 nucleotides" (Claim 37), "at least 150 nucleotides (Claim 38), "at least 25 nucleotides" (Claim 42), and "at least 27 nucleotides" (Claim 43) --are supported in the Specification at least at page 8, lines 3-6, at page 8, line 30 to page 9, line 1, and at page 60, lines 26-29.

Applicants respectfully conclude that no new matter has been entered by the above amendments and new Claims 30-52.

<u>CONCLUSION</u>

Applicants respectfully request that the above amendments to Claims 22-27 of the parent application and and new Claims 30-52 be entered into the instant application. Applicants respectfully submit that the claims as presented are in condition for allowance, and earnestly request their prompt allowance. If the undersigned Attorney for the Applicants can be of any assistance in regard to this <u>Preliminary Amendment</u>, she can be reached at (415) 981-2034.

Respectfully submitted,

Leona L. Lauder
Attorney for Applicants
Registration No. 30,863

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